

The Biogeography and Molecular Diversity of *Mastocarpus papillatus* (Rhodophyta, Phylloporaceae) in Puget Sound, the Strait of Georgia and the Strait of Juan de Fuca

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Mastocarpus papillatus is a common intertidal red alga found along the west coast of North America from Baja California to Alaska, including waters of Puget Sound and the Strait of Georgia. Nuclear ribosomal ITS sequences have revealed that at least five species are included under this single species name. All five of the species occur along the Strait of Juan de Fuca, and three of the species have also been found in the Strait of Georgia and Puget Sound, including the two most geographically widespread species. Few if any morphological characters distinguish the species. In addition to different geographical distributions, the species are differentiated in part by vertical occurrence in the intertidal zone. Two of the species are preferentially found in the mid to high intertidal zone whereas the other three are more common near mean lower low water. The five species exhibit different patterns of haplotype diversity.

Mastocarpus papillatus is a common intertidal red alga found along the west coast of North America from Baja California to Alaska (Abbott & Hollenberg 1976), including waters of Puget Sound, the Strait of Georgia, and the Strait of Juan de Fuca. As Abbott & Hollenberg have noted, it is “probably the most common red alga on the Pacific Coast”. The species has been well-studied in regard to its taxonomy (Abbott 1972), life history (West 1972, Polanshek & West 1975, 1977), and phylogenetic relationships (Fredericq & Lopez-Bautista 2002). Because of this knowledge base and the fact that the species has an alternation of heteromorphic generations, with a macroscopic gametophyte (that gives the species its name), *Mastocarpus papillatus* was chosen to serve as the model organism for assessing patterns of post-glacial recolonization in the marine environment of northern Washington and southern British Columbia (Lindstrom *et al.* 1997).

DNA was extracted from specimens of *Mastocarpus papillatus* collected from the intertidal zone of the Strait of Juan de Fuca, the Strait of Georgia and Puget Sound in 2002 and 2003 using the technique of Lindstrom & Fredericq (2003). The nuclear ribosomal ITS region of the genome was amplified following the protocol of Hughey *et al.* (2001). DNA sequencing was done at the Nucleic Acids Protein Service Unit at the University of British Columbia.

Results revealed five distinct genotype patterns among specimens collected along the southern Vancouver Island shore of the Strait of Juan de Fuca in the spring of 2002. These genotype patterns were interpreted as belonging to separate species because of the lack of intermediate genotypes and because of strong branch support in phylogenetic analyses. Subsequent collections of *Mastocarpus papillatus* in the Strait of Georgia and Puget Sound in 2003 revealed that three of the species (clades 1, 3 and 5) also occurred in these inner waters.

Few if any morphological characters distinguish the species. In addition to sequence differences, the species can be differentiated by their vertical and horizontal distributions. Clades 1 and 2 occur more commonly in the mid to high intertidal zone, and clades 3, 4 and 5 are found near mean lower low water. To date, clade 1 has been found from northern Washington and southern British Columbia (Strait of Juan de Fuca, Puget Sound, and Strait of Georgia) to the eastern Aleutian Islands, clade 2 from northern California to northern Vancouver Island, clade 3 from northern California to northern British Columbia, clade 4 from northern Washington to northern Southeast Alaska, and clade 5 from northern California to the northeast end of the Alaska Peninsula.

The five species exhibit different patterns of haplotype diversity. The genotypes of the three species occurring in local waters include widespread haplotypes: A (distributed from the San Juan Islands to the eastern Aleutian Islands), R (Puget Sound to the Kenai Peninsula), and S (Strait of Juan de Fuca to northern Vancouver Island) in clade 1; A (northern California to the Strait of Juan de Fuca) and C (Bamfield and the Strait of Georgia to northern British Columbia) in clade 3; and A (Strait of Juan de Fuca and Georgia Strait to the northern Alaska Peninsula), E (Strait of Georgia to northern Alaska Peninsula), and J (Strait of Juan de Fuca and Kenai Peninsula) in clade 5. The remaining haplotypes were restricted to the Strait of Juan de Fuca, Strait of Georgia, and/or Puget Sound (see table below).

Haplotypes observed in clades (species) of *Mastocarpus papillatus* in the Strait of Juan de Fuca, Strait of Georgia and Puget Sound.

	Clade 1	Clade 3	Clade 5
Bamfield	—	A, C, D	—
Strait of Juan de Fuca	A, M, R, S, U, W, X, FF, HH	A	A, J, K
Strait of Georgia	R, T, V, Z, AA, BB, DD	C	A, C, E
Puget Sound	R, EE	—	P

Work on *Mastocarpus papillatus* thus far has not provided insight into post-glacial recolonization of the coast, but it has revealed previously undetected and unexpected diversity in the common “Turkish washcloth.” These results provide additional support for the idea that a coastal refugium must have existed in this area during the last Ice Age (Lindstrom *et al.* 1997).

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